

A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
 Tracy A. Willson, et al.
 10/036,568 (11373Z)
 REPLACEMENT SHEET

H		gagtctaacacggaccaaggagttttaac
M	-60	tgaaaagatagaataaatggcctcgtgc
H		M E W P A R L C G
		ATGGAGTGGCCGGCGCGGCTCTGCGGGC
		* * * *
M	1	ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M	1	M A R P A L L G E
H		G G G G A P T E T
H		GGGGGCGGGGGCGCGCCTACGGAAACTC
		* * * *
M	61	GGCCAAGTTGCCGCGGCCACAGAAGTTC
M	21	G Q V A A A T E V
H		E N L C T V I W T
H		GAAAACCTCTGCACAGTAATATGGACAT
		* * * * * * *
M	121	GAAAATCTCTGCACGATAATATGGACGT
M	41	E N L C T I I W T
H		S L W Y F S H F G
H		AGTCTATGGTATTTTAGTCATTTTGGCG
		* * * * *
M	181	ACTCTCAGATATTTTAGTCACTTTGATG
M	61	T L R Y F S H F D

Fig. 7A

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acgtgcggccgggttcgagggcgagaggctgc
.....
cgaattcggcacgagccgagggcgagggcctgc

L W A L L L C A G G G G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGGGGGC
* * * *
TGTTGGTGCTGCTACTGTGGACCGCCACCGTG - - -
L L V L L L W T A T V -

Q P P V T N L S V S V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT
* * * * * * * * * *
AGCCACCTGTGACGAATTTGAGCGTCTCTGTC
Q P P V T N L S V S V

W N P P E G A S S N C
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT
* * * * * * * * * *
GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
W S P P E G A S P N C

D K Q D K K I A P E T
ACAAACAAGATAAGAAAATAGCTCCGGAAACT
* * * * * * * * * *
ACCAACAGGATAAGAAAATTGCTCCAGAAACT
D Q Q D K K I A P E T
    
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Fig. 7B

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H		R	R	S	I	E	V	P	L	N
H		CGTCGTTCAATAGAAGTACCCCTGAATG								
		*		*		*	*			
M	241	CATCGTAAAGAGGAATTACCCCTGGATG								
M	81	H R K E E L P L D								
H		S	T	N	E	S	E	K	P	S
H		AGCACCAATGAGAGTGAGAAGCCTAGCA								
		*	*	*	*	*	*	*	*	*
M	301	AGTGCCAATGAAAGTGAGAAGCCTAGCC								
M	101	S A N E S E K P S								
H		G	D	P	E	S	A	V	T	E
H		GGTGATCCTGAGTCTGCTGTGACTGAAC								
		*	*	*	*	*	*	*	*	*
M	361	GGTGATCCTGAGTCCGCTGTGACTGAGC								
M	121	G D P E S A V T E								
H		K	C	S	W	L	P	G	R	N
H		AAGTGTTCTTGGCTCCCTGGAAGGAATA								
		*	*	*	*	*	*	*	*	*
M	421	AAGTGTTCTTGGCTCCCTGGAAGGAATA								
M	141	K C S W L P G R N								
H		W	H	R	S	L	E	K	I	H
H		TGGCACAGAAGCCTGGAAAAAATTCATC								

Fig. 7C

E R I C L Q V G S Q C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
* * * * *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E K I C L Q V G S Q C

I L V E K C I S P P E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
* * * * *
CTTTGGTGAAAAAGTGCATCTCACCCCCCTGAA
P L V K K C I S P P E

L Q C I W H N L S Y M
TTCAATGCATTTGGCACAACCTGAGCTACATG
* * * * *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L K C I W H N L S Y M

T S P D T N Y T L Y Y
CCAGTCCCGACACTAATACTCTCTACTAT
* * * * *
CAAGCCCTGACACACACTATACTCTGTACTAT
T S P D T H Y T L Y Y

Q C E N I F R E G Q Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC

Fig. 7D

			*		*	*	*	*	
M	481	TGGTACAGCAGCCTGGAGAAAAGTCGTC							
M	161	W Y S S L E K S R							
H		F G C S F D L T K							
H		TTTGGTTGTTTCCTTTGATCTGACCAAAG							
			*	*	*		*	*	*
M	541	ATTGCTTGTTTCCTTTAAATTGACTAAAG							
M	181	I A C S F K L T K							
H		Q I M V K D N A G							
H		CAAATAATGGTCAAGGATAATGCAGGAA							
			*	*	*	*	*	*	*
M	598	CAAATAATGGTCAAGGATAATGCTGGGA							
M	200	Q I M V K D N A G							
H		T S R V K P D P P							
H		ACTTCCC GTGTGAAACCTGATCCTCCAC							
			*	*		*	*	*	*
M	658	ACTTCCTATGTGAAACCTGATCCTCCAC							
M	220	T S Y V K P D P P							
H		L Y V Q W E N P Q							
H		CTATATGTGCAATGGGAGAATCCACAGA							
			*	*	*	*	*	*	*
M	718	TTATTAGTGCAGTGGAAGAATCCACAAA							
M	240	L L V Q W K N P Q							

Fig. 7E

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*   *   *   *   *           *   *   *   *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q   C   E   N   I   Y   R   E   G   Q   H

V   K   D   S   S   F   E   Q   H   S   V
TGAAGGATTCCAGTTTGAACAACACAGTGTC
*               *   *   *               *
TGGAACCT- - -AGTTTTGAACATCAGAACG TT
V   E   P   -   S   F   E   H   Q   N   V

K   I   K   P   S   F   N   I   V   P   L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
*   *           *   *           *   *   *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K   I   R   P   S   C   K   I   V   S   L

H   I   K   N   L   S   F   H   N   D   D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
*   *   *           *               *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H   I   K   H   L   L   L   K   N   G   A

N   F   I   S   R   C   L   F   Y   E   V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
*   *           *   *   *   *           *   *   *
ATTTTAGAAGCAGATGCTTA ACTTATGAAGTG
N   F   R   S   R   C   L   T   Y   E   V
    
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Fig. 7F

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H		E	V	N	N	S	Q	T	E	T
H		GAAGTCAATAACAGCCAAACTGAGACAC								
		*	*	*	*	*	*			
M	778	GAGGTCAATAATACTCAAACCGACCGAC								
M	260	E	V	N	N	T	Q	T	D	R
H		E	N	P	E	F	E	R	N	V
H		GAGAATCCAGAATTTGAGAGAAATGTGG								
		*		*			*	*		
M	838	CAGAATTCCGAATCTGATAGAAACATGG								
M	280	Q	N	S	E	S	D	R	N	M
H		L	P	D	T	L	N	T	V	R
H		CTTCCTGATACTTTGAACACAGTCAGAA								
		*		*			*	*	*	
M	898	CTTGCCGACGCTGTCTACACAGTCAGAG								
M	300	L	A	D	A	V	Y	T	V	R
H		D	D	K	L	W	S	N	W	S
H		GATGACAAACTCTGGAGTAATTGGAGCC								
		*		*	*	*	*	*	*	
M	958	GACAACAAACTGTGGAGTGATTGGAGTG								
M	320	D	N	K	L	W	S	D	W	S
H		T	L	Y	I	T	M	L	L	I
H		AACTCTACATAACCATGTTACTCATTG								

Fig. 7G

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H N V F Y V Q E A K C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
* * * * *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H N I L E V E E D K C

E N T S C F M V P G V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
* * * * *
AGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT
E G T S C F Q L P G V

I R V K T N K L C Y E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
* * * * *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V R V K T N K L C F D

Q E M S I G K K R N S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
* * * * *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E A Q S I G K E Q N S

V P V I V A G A I I V
TTCCAGTCATCGTCGCAGGTGCAATCATAGTA

Fig. 7H

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		*		*		*		*		*		*		*													
M	1018	A	C	C	T	T	C	T	A	C	C	A	C	C	A	T	G	T	T	A	C	T	C	A	C	C	A
M	340	T	F	Y	T	T	M	L	L	T																	
H		L	L	L	Y	L	K	R	L	K																	
H		C	T	C	T	G	C	T	T	A	C	T	A	A	A	A	G	G	C	T	C	A	A	G	A		
		*	*		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
M	1078	C	T	C	T	T	T	T	A	C	T	G	A	A	A	A	G	G	C	T	T	A	A	G	A		
M	360	L	L	F	Y	L	K	R	L	K																	
H		K	I	F	K	E	M	F	G	D																	
H		A	A	G	A	T	T	T	T	T	A	A	G	A	A	A	T	G	T	T	T	G	G	A	G	A	C
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
M	1138	A	A	G	A	T	T	T	T	T	A	A	G	A	A	A	T	G	T	T	T	G	G	A	G	A	C
M	380	K	I	F	K	E	M	F	G	D																	
H		D	I	Y	E	K	Q	T	K	E																	
H		G	A	C	A	T	C	T	A	T	G	A	G	A	A	C	C	A	A	G	G	A	G	A	G	A	G
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
M	1198	G	A	C	A	T	C	T	A	T	G	A	G	A	A	C	A	A	T	C	C	A	A	G	A	A	G
M	400	D	I	Y	E	K	Q	S	K	E																	
H		K	K	A	S	Q	*																				
H		A	A	G	A	A	G	C	C	T	C	T	C	A	G	T	G	A	t	g	g	a	a	t	a	a	t
		*	*	*																							
M	1258	A	A	G	A	A	G	C	A	G	C	T	C	C	T	T	G	A	t	g	g	g	a	a	a	a	g
M	420	K	K	A	A	P	*																				

Fig. 7I

```

      *   *       *   *       *       *
TTCCAGTCTTTGTCGCGAGTGGCAGTCATAATC
I   P   V   F   V   A   V   A   V   I   I

I   I   I   F   P   P   I   P   D   P   G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
*   *   *   *   *   *   *   *   *   *
TCATTATATTTCCCTCCAATTCCTGATCCTGGC
I   I   I   F   P   P   I   P   D   P   G

Q   N   D   D   T   L   H   W   K   K   Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
*   *   *   *   *   *   *   *   *   *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q   N   D   D   T   L   H   W   K   K   Y

E   T   D   S   V   V   L   I   E   N   L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
*   *   *   *   *   *   *   *   *   *
AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E   T   D   S   V   V   L   I   E   N   L

ttattttttaccttcactgtgaccttgagaaga
tgattttctttcttgccttcaatgtgaccctgt
    
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Fig. 7J